

PATENT
Attorney Docket No.:28967/34891A

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Alitalo *et al.*) EXPRESS MAIL LABEL NO.:
Serial No.: Not yet assigned) EM578445010US
Filed: Herewith)) I hereby certify that this paper and
For: Flt4 (VEGFR-3) as a Target) the documents referred to as
for Tumor Imaging and Anti-Tumor) enclosed herewith are being
Therapy) deposited with the United States
Group Art Unit: Not yet assigned) Postal Service as "EXPRESS MAIL
Examiner: Not yet assigned) POST OFFICE TO ADDRESSEE"
) Service under 37 C.F.R. §1.10 on
) the date indicated below and is
) addressed to: Commissioner for
) Patents, Box Patent Application,
) Washington, D.C. 20231 on this
) date:
) January 19, 2001
) 
) David A. Gass

STATEMENT PURSUANT TO 37 C.F.R. § 1.921(f)

Commissioner for Patents
Box Patent Application
Washington, D.C. 20231

Sir:

I hereby state that the content of the paper and computer readable forms of the sequence listing that is part of the above-identified application and that are filed herewith are the same.

Respectfully submitted,

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January 19, 2001

By:


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Reg. No: 38,153

SEQUENCE LISTING

<110> Alitalo, Kari
Kaipainen, Arja
Valtola, Reija
Jussila, Lotta

<120> Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therapy

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Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu
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Val Asn Val Ser Asp Ser Leu Glu Met Gln Cys Leu Val Ala Gly Ala
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Ile Ala Val Phe Phe Trp Val Leu Leu Leu Ile Phe Cys Asn Met
785 790 795 800

Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly Tyr Leu Ser Ile Ile
805 810 815

Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln Cys Glu Tyr Leu Ser
820 825 830

Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu Arg Leu His Leu Gly
835 840 845

Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val Val Glu Ala Ser Ala
850 855 860

Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr Val Ala Val Lys Met
865 870 875 880

Leu Lys Glu Gly Ala Thr Ala Ser Glu His Arg Ala Leu Met Ser Glu
885 890 895

Leu Lys Ile Leu Ile His Ile Gly Asn His Leu Asn Val Val Asn Leu
900 905 910

Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu Met Val Ile Val Glu
915 920 925

Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu Arg Ala Lys Arg Asp
930 935 940

Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu Gln Arg Gly Arg Phe
945 950 955 960

Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg Arg Arg Pro Gly Ser
965 970 975

Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys Thr Glu Gly Gly Ala
980 985 990

Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp Leu Trp Leu Ser Pro
995 1000 1005

Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe Gln Val Ala Arg Gly
1010 1015 1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
025 1030 1035 1040

Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe
1045 1050 1055

Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
1060 1065 1070

Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp
1075 1080 1085

Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu
1090 1095 1100

Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile
105 1110 1115 1120

Asn Glu Glu Phe Cys Gln Arg Leu Arg Asp Gly Thr Arg Met Arg Ala
1125 1130 1135

Pro Glu Leu Ala Thr Pro Ala Ile Arg Arg Ile Met Leu Asn Cys Trp
1140 1145 1150

Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Glu Leu Val Glu Ile
1155 1160 1165

Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Val
1170 1175 1180

Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser
185 1190 1195 1200

Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp
1205 1210 1215

Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn
1220 1225 1230

Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly
1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr
1250 1255 1260

Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
265 1270 1275 1280

Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val Thr Arg Ala His
1300 1305 1310

Pro Asp Ser Gln Gly Arg Arg Arg Pro Glu Arg Gly Ala Arg Gly
1315 1320 1325

Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu Ser Glu Pro Ser
1330 1335 1340

Glu Glu Asp His Cys Ser Pro Ser Ala Arg Val Thr Phe Phe Thr Asp
345 1350 1355 1360

Asn Ser Tyr

<210> 5
<211> 1311
<212> PRT
<213> Homo sapiens (FLT1)

<400> 5
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Asn Asn Asn Asn Asn Met Val Ser Lys Glu Ser Glu Arg Leu
65 70 75 80

Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser
85 90 95

Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser
100 105 110

Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser
115 120 125

Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met
130 135 140

Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu
145 150 155 160

Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys
165 170 175

Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp
180 185 190

Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile
195 200 205

Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr
210 215 220

Asn Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln
225 230 235 240

Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val
245 250 255

Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr
260 265 270

Trp Ser Tyr Pro Asp Asn Asn Glu Lys Asn Lys Arg Ala Ser Val
275 280 285

Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser
290 295 300

Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr
305 310 315 320

Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val
325 330 335

His Ile Tyr Asp Lys Ala Phe Ile Thr Val Lys His Arg Lys Gln Gln
340 345 350

Val Leu Glu Thr Val Ala Gly Lys Arg Ser Tyr Arg Leu Ser Met Lys
355 360 365

Val Lys Ala Phe Pro Ser Pro Glu Val Val Trp Leu Lys Asp Gly Leu
370 375 380

Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu Thr Arg Gly Tyr Ser Leu
385 390 395 400

Ile Ile Lys Asp Val Thr Glu Glu Asp Ala Gly Asn Tyr Thr Ile Leu
405 410 415

Leu Ser Ile Lys Gln Ser Asn Val Phe Lys Asn Leu Thr Ala Thr Leu
420 425 430

Ile Val Asn Val Lys Pro Gln Ile Tyr Glu Lys Ala Val Ser Ser Phe
435 440 445

Pro Asp Pro Ala Leu Tyr Pro Leu Gly Ser Arg Gln Ile Leu Thr Cys
450 455 460

Thr Ala Tyr Gly Ile Pro Gln Pro Asn Thr Ile Lys Trp Phe Trp His
465 470 475 480

Pro Cys Asn His Asn His Ser Glu Ala Arg Cys Asp Phe Cys Ser Asn
485 490 495

Asn Glu Glu Ser Phe Ile Leu Asp Asn Asn Asn Asn Asn Asn Ala
500 505 510

Asp Ser Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala
515 520 525

Ile Ile Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp
530 535 540

Ser Arg Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly
545 550 555 560

Thr Val Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly
565 570 575

Phe His Val Asn Leu Glu Lys Met Pro Thr Asn Asn Glu Gly Glu Asp
580 585 590

Leu Lys Leu Ser Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr
595 600 605

Trp Ile Leu Leu Asn
610 615 620

Asn Asn Asn Asn Asn Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser
625 630 635 640

Ile Ser Lys Gln Lys Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu
645 650 655

Asn Leu Thr Ile Met Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala
660 665 670

Cys Arg Ala Arg Asn Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys
675 680 685

Glu Ile Thr Ile Arg Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu
690 695 700

Ser Asp His Thr Val Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His
705 710 715 720

Ala Asn Gly Val Pro Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His
725 730 735

Lys Ile Gln Gln Glu Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr
740 745 750

Leu Phe Ile Glu Arg Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys
755 760 765

Lys Ala Thr Asn Gln Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr
770 775 780

Val Gln Gly Thr Ser Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr
785 790 795 800

Cys Thr Cys Val Ala Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu
805 810 815

Ile Arg Lys Met Lys Arg Ser Ser Asn Ser Glu Ile Lys Thr Asp Tyr
820 825 830

Leu Ser Ile Ile Met Asp Pro Asp Glu Val Pro Leu Asp Glu Gln Cys
835 840 845

Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg
850 855 860

Leu Lys Leu Gly Lys Ser Leu Gly Arg Gly Ala Phe Gly Lys Val Val
865 870 875 880

Gln Ala Ser Ala Phe Gly Ile Lys Lys Ser Pro Thr Cys Arg Thr Val
885 890 895

Ala Val Lys Met Leu Lys Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala
900 905 910

Leu Met Thr Glu Leu Lys Ile Leu Thr His Ile Gly His His Leu Asn
915 920 925

Val Val Asn Leu Leu Gly Ala Cys Thr Lys Gln Gly Pro Leu Met
930 935 940

Val Ile Val Glu Tyr Cys Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys
945 950 955 960

Ser Lys Arg Asp Leu Phe Phe Leu Asn Lys Asp Ala Ala Leu His Met
965 970 975

Glu Pro Lys Lys Glu Lys Met Glu Pro Gly Leu Glu Gln Gly Lys Lys
980 985 990

Pro Arg Leu Asp Ser Val Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly
995 1000 1005

Phe Gln Glu Asp Lys Ser Leu Ser Asp Val Glu Glu Glu Asp Ser
1010 1015 1020

Asp Gly Phe Tyr Lys Glu Pro Ile Thr Met Glu Asp Leu Ile Ser Tyr
1025 1030 1035 1040

Ser Phe Gln Val Ala Arg Gly Met Glu Phe Leu Ser Ser Arg Lys Cys
1045 1050 1055

Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Asn Asn
1060 1065 1070

Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asn
1075 1080 1085

Pro Asp Tyr Val Arg Lys Gly Asp Thr Arg Leu Pro Leu Lys Trp Met
1090 1095 1100

Ala Pro Glu Ser Ile Phe Asp Lys Ile Tyr Ser Thr Lys Ser Asp Val
1105 1110 1115 1120

Trp Ser Tyr Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Ser
1125 1130 1135

Pro Tyr Pro Gly Val Gln Met Asp Glu Asp Phe Cys Ser Arg Leu Arg
1140 1145 1150

Glu Gly Met Arg Met Arg Ala Pro Glu Tyr Ser Thr Pro Glu Ile Tyr
1155 1160 1165

Gln Ile Met Leu Asp Cys Trp His Arg Asp Pro Lys Glu Arg Pro Arg
1170 1175 1180

Phe Ala Glu Leu Val Glu Lys Leu Gly Asp Leu Leu Gln Ala Asn Val
1185 1190 1195 1200

Gln Gln Asp Gly Lys Asp Tyr Ile Pro Ile Asn Ala Ile Leu Thr Gly
1205 1210 1215

Asn Ser Gly Phe Thr Tyr Ser Thr Pro Ala Phe Ser Glu Asp Phe Phe
1220 1225 1230

Lys Glu Ser Ile Ser Ala Pro Lys Phe Asn Ser Gly Ser Ser Asp Asp
1235 1240 1245

Val Arg Tyr Val Asn Ala Phe Lys Phe Met Ser Leu Glu Arg Ile Lys
1250 1255 1260

Thr Phe Glu Glu Leu Leu Pro Asn Ala Thr Ser Met Phe Asp Asp Tyr
1265 1270 1275 1280

Gln Gly Asp Ser Ser Thr Leu Leu Ala Ser Pro Met Leu Lys Arg Phe
1285 1290 1295

Thr Trp Thr Asp Ser Lys Pro Lys Ala Ser Leu Lys Ile Glu Val
1300 1305 1310

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> The amino acid at positions 1 and 2 each are selected independently from the group consisting of aspartic acid and glutamic acid.

<220>

<223> The amino acid at position 4 is independently selected from the group consisting of methionine and valine.

<220>
<223> The amino acid at position 5 is independently selected from the group consisting of proline, aspartic acid, and glutamic acid.

<220>
<223> Description of Artificial Sequence: consensus sequence

<400> 6
Xaa Xaa Tyr Xaa Xaa Met
1 5

<210> 7
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 7
acatgcatgc caccatgcag cggggcgccg cgctgtgcct gcgactgtgg ctctgcctgg 60
gactcctgga 70

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 8
acatgcatgc cccgccggtc atcc 24

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 9
cggaattccc catgacccca ac 22

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide probe

<400> 10
ccatcgatgg atcctacctg aagccgcttt ctt

33

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide probe

<400> 11
ccccaaaggcttg gatccaaagtg gctactccat gacc

34

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide probe

<400> 12
gttgcctgtg atgtgcacca

20

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide probe

<400> 13
ctggagtcga cttggcggac t

21

<210> 14
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide probe

<400> 14
cgcggatccc tagtgatggat gatgggtatg tctacacctcg atcatgtgc ccttatacctc 60

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 15
ctggagtcga cttggcggac t 21

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 16
cgggatccct ccatgctgcc cttatcct 28

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 17
ggcaagcttg aattcgccac catgcagcgg ggcgcc 36

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 18
gttgcctgtg atgtgcacca 20

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 19
ctggagtcga cttggcggac t 21

<210> 20
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 20
cgccggatcca agcttactta ccttccatgc tgcccttatac ctgc 44

<210> 21
<211> 419
<212> PRT
<213> Homo sapiens

<400> 21
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
405 410 415

Gln Met Ser

<210> 22
<211> 354
<212> PRT
<213> Homo sapiens

<400> 22
Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
1 5 10 15

Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
20 25 30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35 40 45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

sn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
165 170 175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
180 185 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
195 200 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
210 215 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225 230 235 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
260 265 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
290 295 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
305 310 315 320

His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
325 330 335

Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
340 345 350

Asn Pro